SEQUENCE LISTING

<110> SEIKI, Motoharu
      SATO, Hiroshi
      SHINAGAWA, Akira

<120> NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR

<130> 55-290P

<140> 08/448,489
<141> 1995-06-07

<160> 19

<170> PatentIn Ver. 2.0

<210> 1
<211> 582
<212> PRT
<213> Homo sapiens

<400> 1

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Phe Ser Pro Glu Ala Trp Leu Gln Gln Tyr Gly Tyr Leu Pro Pro Gly
            35                  40                  45

Asp Leu Arg Thr His Thr Gln Arg Ser Pro Gln Ser Leu Ser Ala Ala
        50                  55                  60

Ile Ala Ala Met Gln Lys Phe Tyr Gly Leu Gln Val Thr Gly Lys Ala
    65                  70                  75                  80

Asp Ala Asp Thr Met Lys Ala Met Arg Arg Pro Arg Cys Gly Val Pro
                85                  90                  95

Asp Lys Phe Gly Ala Glu Ile Lys Ala Asn Val Arg Arg Lys Arg Tyr
                100                 105                 110

Ala Ile Gln Gly Leu Lys Trp Gln His Asn Glu Ile Thr Phe Cys Ile
                115                 120                 125

Gln Asn Tyr Thr Pro Lys Val Gly Glu Tyr Ala Thr Tyr Glu Ala Ile
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1

Arg Lys Ala Phe Arg Val Trp Glu Ser Ala Thr Pro Leu Arg Phe Arg
145   150   155   160

Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp
                165   170   175

Ile Met Ile Phe Phe Ala Glu Gly Phe His Gly Asp Ser Thr Pro Phe
                180   185   190

Asp Gly Glu Gly Gly Phe Leu Ala His Ala Tyr Phe Pro Gly Pro Asn
                195   200   205

Ile Gly Gly Asp Thr His Phe Asp Ser Ala Glu Pro Trp Thr Val Arg
            210   215   220

Asn Glu Asp Leu Asn Gly Asn Asp Ile Phe Leu Val Ala Val His Glu
225   230   235   240

Leu Gly His Ala Leu Gly Leu Glu His Ser Ser Asp Pro Ser Ala Ile
                245   250   255

Met Ala Pro Phe Tyr Gln Trp Met Asp Thr Glu Asn Phe Val Leu Pro
                260   265   270

Asp Asp Asp Arg Arg Gly Ile Gln Gln Leu Tyr Gly Gly Glu Ser Gly
            275   280   285

Phe Pro Thr Lys Met Pro Pro Gln Pro Arg Thr Thr Ser Arg Pro Ser
    290   295   300

Val Pro Asp Lys Pro Lys Asn Pro Thr Tyr Gly Pro Asn Ile Cys Asp
305   310   315   320

Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met Phe Val Phe
                325   330   335

Lys Lys Arg Trp Phe Trp Arg Val Arg Asn Asn Gln Val Met Asp Gly
            340   345   350

Tyr Pro Met Pro Ile Gly Gln Phe Trp Arg Gly Leu Pro Ala Ser Ile
        355   360   365

Asn Thr Ala Tyr Glu Arg Lys Asp Gly Lys Phe Val Phe Phe Lys Gly
    370   375   380

Asp Lys His Trp Val Phe Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro

2

Lys His Ile Lys Glu Leu Gly Arg Gly Leu Pro Thr Asp Lys Ile Asp
            405   410   415

Ala Ala Leu Phe Trp Met Pro Asn Gly Lys Thr Tyr Phe Phe Arg Gly
            420   425   430

Asn Lys Tyr Tyr Arg Phe Asn Glu Glu Leu Arg Ala Val Asp Ser Glu
            435   440   445

Tyr Pro Lys Asn Ile Lys Val Trp Glu Gly Ile Pro Glu Ser Pro Arg
      450   455   460

Gly Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys Gly
465   470   475   480

Asn Lys Tyr Trp Lys Phe Asn Asn Gln Lys Leu Lys Val Glu Pro Gly
            485   490   495

Tyr Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
            500   505   510

Arg Pro Asp Glu Gly Thr Glu Glu Glu Thr Glu Val Ile Ile Ile Glu
            515   520   525

Val Asp Glu Glu Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu
      530   535   540

Pro Val Leu Leu Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe
545   550   555   560

Phe Phe Arg Arg His Gly Thr Pro Arg Arg Leu Leu Tyr Cys Gln Arg
            565   570   575

Ser Leu Leu Asp Lys Val
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<210> 2
<211> 3403
<212> DNA
<213> Homo sapiens

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3

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gccatcgctg ccatgcagaa gttttacggc ttgcaagtaa caggcaaagc tgatgcagac 360
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aaggccaatg ttcgaaggaa gcgctacgcc atccagggtc tcaaatggca acataatgaa 480
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4

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cggcctgctc accatctcag tgagggacag gagctggggc tgcttaggct gggtccacgc 3120
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acccagccca cccattgaag tctccttggg tcccaaaggt gggcatggta ccgggggactt 3240
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<210> 3
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Highly conserved
      sequence fragments from MMP family

<400> 3
Pro Arg Cys Gly Val Pro Asp
  1   5

<210> 4
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Highly conserved
      sequence fragments from MMP family

<400> 4
Gly Asp Ala His Phe Asp Asp Asp Glu
  1   5

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 5
ccmmgvtgys gvrwbccwga   20

<210> 6
<211> 25

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 6
ytcrtsvtcr tcraartgrr hrtcy                                          25

<210> 7
<211> 30
<212> PRT
<213> Homo sapiens

<400> 7
Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu Pro Val Leu Leu
 1               5               10              15

Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe Phe Phe
            20              25              30

<210> 8
<211> 14
<212> PRT
<213> Homo sapiens

<400> 8
Arg Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys
 1               5               10

<210> 9
<211> 14
<212> PRT
<213> Homo sapiens

<400> 9
Asp Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met
 1               5               10

<210> 10
<211> 15
<212> PRT
<213> Homo sapiens

<400> 10

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Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
 1               5                  10                 15
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<210> 11
<211> 489
<212> PRT
<213> Unknown

<220>
<223> X = UNKNOWN

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 11
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Met Ala Pro Ala Ala Trp Leu Arg Ser Ala Ala Ala Arg Ala Leu Leu
 1               5                  10                 15

Pro Pro Met Leu Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg
            20                  25                  30

Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro
            35                  40                  45

Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala
        50                  55                  60

Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys
65                  70                  75                  80

Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys
                85                  90                  95

Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr
            100                 105                 110

Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln
            115                 120                 125

Thr Met Ala Glu Ala Leu Lys Val Trp Ser Asp Val Thr Pro Leu Thr
            130                 135                 140

Phe Thr Glu Val His Glu Gly Arg Ala Asp Ile Met Ile Asp Phe Ala
145                 150                 155                 160

Arg Tyr Trp Asp Gly Asp Asp Leu Pro Phe Asp Gly Pro Gly Gly Ile
```

Leu Ala His Ala Phe Phe Pro Lys Thr His Arg Glu Gly Asp Val His
        180   185   190

Phe Asp Tyr Asp Glu Thr Trp Thr Ile Gly Asp Asp Gln Gly Thr Asp
        195   200   205

Leu Leu Gln Val Ala Ala His Glu Phe Gly His Val Leu Gly Leu Gln
        210   215   220

His Thr Thr Ala Ala Lys Ala Leu Met Ser Ala Phe Tyr Thr Phe Arg
225   230   235   240

Tyr Pro Leu Ser Leu Ser Pro Asp Asp Cys Arg Gly Val Gln His Leu
        245   250   255

Tyr Gly Gln Pro Trp Pro Thr Val Thr Ser Arg Thr Pro Ala Leu Gly
        260   265   270

Pro Gln Ala Gly Ile Asp Thr Asn Glu Ile Ala Pro Leu Glu Pro Asp
        275   280   285

Ala Pro Pro Asp Ala Cys Glu Ala Ser Phe Asp Ala Val Ser Thr Ile
        290   295   300

Arg Gly Glu Leu Phe Phe Phe Lys Ala Gly Phe Val Trp Arg Leu Arg
305   310   315   320

Gly Gly Gln Leu Gln Pro Gly Tyr Pro Ala Leu Ala Ser Arg His Trp
        325   330   335

Gln Gly Leu Pro Ser Pro Val Asp Ala Ala Phe Glu Asp Ala Gln Gly
        340   345   350

His Ile Trp Phe Phe Gln Gly Ala Gln Tyr Trp Val Tyr Asp Gly Glu
        355   360   365

Lys Pro Val Leu Gly Pro Ala Pro Leu Thr Glu Leu Gly Leu Val Arg
        370   375   380

Phe Pro Val His Ala Ala Leu Val Trp Gly Pro Glu Lys Asn Lys Ile
385   390   395   400

Tyr Phe Phe Arg Gly Arg Asp Tyr Trp Arg Phe His Pro Ser Thr Arg
        405   410   415

Arg Val Asp Ser Pro Val Pro Arg Arg Ala Thr Asp Trp Arg Gly Val

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                 420                      425                      430
Pro Ser Glu Ile Asp Ala Ala Phe Gln Asp Ala Asp Gly Tyr Ala Tyr
         435                      440                      445
Phe Leu Arg Gly Arg Leu Tyr Trp Lys Phe Asp Pro Val Lys Val Lys
         450                      455                      460
Ala Leu Glu Gly Phe Pro Arg Leu Val Gly Pro Asp Phe Phe Gly Cys
465                      470                      475                      480
Ala Glu Pro Ala Asn Thr Phe Leu Xaa
                 485
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<210> 12
<211> 469
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 12
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Met His Ser Phe Pro Pro Leu Leu Leu Leu Phe Trp Gly Val Val
  1               5                  10                  15
Ser His Ser Phe Pro Ala Thr Leu Glu Thr Gln Glu Gln Asp Val Asp
             20                  25                  30
Leu Val Gln Lys Tyr Leu Glu Lys Tyr Tyr Asn Leu Lys Asn Asp Gly
         35                  40                  45
Arg Gln Val Glu Lys Arg Arg Asn Ser Gly Pro Val Val Glu Lys Leu
         50                  55                  60
Lys Gln Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp
65                  70                  75                  80
Ala Glu Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp
             85                  90                  95
Val Ala Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr
             100                 105                 110
His Leu Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala
         115                 120                 125
```

9

Asp Val Asp His Ala Ile Glu Lys Ala Phe Gln Leu Trp Ser Asn Val
    130   135   140

Thr Pro Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met
145   150   155   160

Ile Ser Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly
                165   170   175

Pro Gly Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly
                180   185   190

Gly Asp Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Thr
                195   200   205

Glu Tyr Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu
    210   215   220

Gly Leu Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr
225   230   235   240

Thr Phe Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile
                245   250   255

Gln Ala Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro
                260   265   270

Gln Thr Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr
                275   280   285

Thr Ile Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg
    290   295   300

Thr Asn Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Thr Ser Val Phe
305   310   315   320

Trp Pro Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp
                325   330   335

Arg Asp Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln
                340   345   350

Gly Gln Asn Val Leu His Gly Tyr Pro Lys Asp Ile Tyr Ser Ser Phe
    355   360   365

Gly Phe Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu
    370   375   380

10

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Asn Thr Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr
385                 390             395             400

Asp Glu Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala
            405             410             415

His Asp Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys
            420             425             430

Asp Gly Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp
        435             440             445

Pro Lys Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe
    450             455             460

Asn Cys Arg Lys Asn
465


<210> 13
<211> 468
<212> PRT
<213> Unknown

<220>
<223> X = UNKNOWN

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 13
Met Phe Ser Leu Lys Thr Leu Pro Phe Leu Leu Leu Leu His Val Gln
  1             5               10              15

Ile Ser Lys Ala Phe Pro Val Ser Ser Lys Glu Lys Asn Thr Lys Thr
            20              25              30

Val Gln Asp Tyr Leu Glu Lys Phe Tyr Gln Leu Pro Ser Asn Gln Tyr
        35              40              45

Gln Ser Thr Arg Lys Asn Gly Thr Asn Val Ile Val Glu Lys Leu Lys
    50              55              60

Glu Met Gln Arg Phe Phe Gly Leu Asn Val Thr Gly Lys Pro Asn Glu
 65             70              75              80
```

11

Glu Thr Leu Asp Met Met Lys Lys Pro Arg Cys Gly Val Pro Asp Ser
                85   90   95

Gly Gly Phe Met Leu Thr Pro Gly Asn Pro Lys Trp Glu Arg Thr Asn
               100   105   110

Leu Thr Tyr Arg Ile Arg Asn Tyr Thr Pro Gln Leu Ser Glu Ala Glu
           115   120   125

Val Glu Arg Ala Ile Lys Asp Ala Phe Glu Leu Trp Ser Val Ala Ser
       130   135   140

Pro Leu Ile Phe Thr Arg Ile Ser Gln Gly Glu Ala Asp Ile Asn Ile
145   150   155   160

Ala Phe Tyr Gln Arg Asp His Gly Asp Asn Ser Pro Phe Asp Gly Pro
               165   170   175

Asn Gly Ile Leu Ala His Ala Phe Gln Pro Gly Gln Gly Ile Gly Gly
           180   185   190

Asp Ala His Phe Asp Ala Glu Glu Thr Trp Thr Asn Thr Ser Ala Asn
       195   200   205

Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ser Leu Gly
   210   215   220

Leu Ala His Ser Ser Asp Pro Gly Ala Leu Met Tyr Pro Asn Tyr Ala
225   230   235   240

Phe Arg Glu Thr Ser Asn Tyr Ser Leu Pro Gln Asp Asp Ile Asp Gly
               245   250   255

Ile Gln Ala Ile Tyr Gly Leu Ser Ser Asn Pro Ile Gln Pro Thr Gly
           260   265   270

Pro Ser Thr Pro Lys Pro Cys Asp Pro Ser Leu Thr Phe Asp Ala Ile
       275   280   285

Thr Thr Leu Arg Gly Glu Ile Leu Phe Phe Lys Asp Arg Tyr Phe Trp
   290   295   300

Arg Arg His Pro Gln Leu Gln Arg Val Glu Met Asn Phe Ile Ser Leu
305   310   315   320

Phe Trp Pro Ser Leu Pro Thr Gly Ile Gln Ala Ala Tyr Glu Asp Phe
               325   330   335

12

Asp Arg Asp Leu Ile Phe Leu Phe Lys Gly Asn Gln Tyr Trp Ala Leu
        340   345   350

Ser Gly Tyr Asp Ile Leu Gln Gly Tyr Pro Lys Asp Ile Ser Asn Tyr
        355   360   365

Gly Phe Pro Ser Ser Val Gln Ala Ile Asp Ala Ala Val Phe Tyr Arg
        370   375   380

Ser Lys Thr Tyr Phe Phe Val Asn Asp Gln Phe Trp Arg Tyr Asp Asn
385   390   395   400

Gln Arg Gln Phe Met Glu Pro Gly Tyr Pro Lys Ser Ile Ser Gly Ala
                405   410   415

Phe Pro Gly Ile Glu Ser Lys Val Asp Ala Val Phe Gln Gln Glu His
                420   425   430

Phe Phe His Val Phe Ser Gly Pro Arg Tyr Tyr Ala Phe Asp Leu Ile
                435   440   445

Ala Gln Arg Val Thr Arg Val Ala Arg Gly Asn Lys Trp Leu Asn Cys
        450   455   460

Arg Tyr Gly Xaa
465

<210> 14
<211> 476
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 14
Met Met His Leu Ala Phe Leu Val Leu Leu Cys Leu Pro Val Cys Ser
  1   5   10   15

Ala Tyr Pro Leu Ser Gly Ala Ala Lys Glu Glu Asp Ser Asn Lys Asp
              20   25   30

Leu Ala Gln Gln Tyr Leu Glu Lys Tyr Tyr Asn Leu Glu Lys Asp Val
          35   40   45

Lys Gln Phe Arg Arg Lys Asp Ser Asn Leu Ile Val Lys Lys Ile Gln

13

Gly Met Gln Lys Phe Leu Gly Leu Glu Val Thr Gly Lys Leu Asp Thr
65   70   75   80

Asp Thr Leu Glu Val Met Arg Lys Pro Arg Cys Gly Val Pro Asp Val
                85   90   95

Gly His Phe Ser Ser Phe Pro Gly Met Pro Lys Trp Arg Lys Thr His
                100   105   110

Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Asp Ala
                115   120   125

Val Asp Ser Ala Ile Glu Lys Ala Leu Lys Val Trp Glu Glu Val Thr
        130   135   140

Pro Leu Thr Phe Ser Arg Leu Tyr Glu Gly Glu Ala Asp Ile Met Ile
145   150   155   160

Ser Phe Ala Val Lys Glu His Gly Asp Phe Tyr Ser Phe Asp Gly Pro
                165   170   175

Gly His Ser Leu Ala His Ala Tyr Pro Pro Gly Pro Gly Leu Tyr Gly
                180   185   190

Asp Ile His Phe Asp Asp Asp Glu Lys Trp Thr Glu Asp Ala Ser Gly
                195   200   205

Thr Asn Leu Phe Leu Val Ala Ala His Glu Leu Gly His Ser Leu Gly
        210   215   220

Leu Phe His Ser Ala Asn Thr Glu Ala Leu Met Tyr Pro Leu Tyr Asn
225   230   235   240

Ser Phe Thr Glu Leu Ala Gln Phe Arg Leu Ser Gln Asp Asp Val Asn
                245   250   255

Gly Ile Gln Ser Leu Tyr Gly Pro Pro Pro Ala Ser Thr Glu Glu Pro
                260   265   270

Leu Val Pro Thr Lys Ser Val Pro Ser Gly Ser Glu Met Pro Ala Lys
        275   280   285

Cys Asp Pro Ala Leu Ser Phe Asp Ala Ile Ser Thr Leu Arg Gly Glu
        290   295   300

Tyr Leu Phe Phe Lys Asp Arg Tyr Phe Trp Arg Arg Ser His Trp Asn

14

Pro Glu Pro Glu Phe His Leu Ile Ser Ala Phe Trp Pro Ser Leu Pro
                325   330   335

Ser Tyr Leu Asp Ala Ala Tyr Glu Val Asn Ser Arg Asp Thr Val Phe
                340   345   350

Ile Phe Lys Gly Asn Glu Phe Trp Ala Ile Arg Gly Asn Glu Val Gln
                355   360   365

Ala Gly Tyr Pro Arg Gly Ile His Thr Leu Gly Phe Pro Pro Thr Ile
                370   375   380

Arg Lys Ile Asp Ala Ala Val Ser Asp Lys Glu Lys Lys Lys Thr Tyr
385   390   395   400

Phe Phe Ala Ala Asp Lys Tyr Trp Arg Phe Asp Glu Asn Ser Gln Ser
                405   410   415

Met Glu Gln Gly Phe Pro Arg Leu Ile Ala Asp Asp Phe Pro Gly Val
                420   425   430

Glu Pro Lys Val Asp Ala Val Leu Gln Ala Phe Gly Phe Phe Tyr Phe
                435   440   445

Phe Ser Gly Ser Ser Gln Phe Glu Phe Asp Pro Asn Ala Arg Met Val
                450   455   460

Thr His Ile Leu Lys Ser Asn Ser Trp Leu His Cys
465   470   475

<210> 15
<211> 477
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 15
Met Lys Ser Leu Pro Ile Leu Leu Leu Leu Cys Val Ala Val Cys Ser
  1   5   10   15

Ala Tyr Pro Leu Asp Gly Ala Ala Arg Gly Glu Asp Thr Ser Met Asn
                20   25   30

15

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Leu Val Gln Lys Tyr Leu Glu Asn Tyr Tyr Asp Leu Lys Lys Asp Val
        35                  40                  45

Lys Gln Phe Val Arg Arg Lys Asp Ser Gly Pro Val Val Lys Lys Ile
        50                  55                  60

Arg Glu Met Gln Lys Phe Leu Gly Leu Glu Val Thr Gly Lys Leu Asp
65                  70                  75                  80

Ser Asp Thr Leu Glu Val Met Arg Lys Pro Arg Cys Gly Val Pro Asp
                85                  90                  95

Val Gly His Phe Arg Thr Phe Pro Gly Ile Pro Lys Trp Arg Lys Thr
                100                 105                 110

His Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Lys Asp
                115                 120                 125

Ala Val Asp Ser Ala Val Glu Lys Ala Leu Lys Val Trp Glu Glu Val
        130                 135                 140

Thr Pro Leu Thr Phe Ser Arg Leu Tyr Glu Gly Glu Ala Asp Ile Met
145                 150                 155                 160

Ile Ser Phe Ala Val Arg Glu His Gly Asp Phe Tyr Pro Phe Asp Gly
                165                 170                 175

Pro Gly Asn Val Leu Ala His Ala Tyr Ala Pro Gly Pro Gly Ile Asn
                180                 185                 190

Gly Asp Ala His Phe Asp Asp Asp Glu Gln Trp Thr Lys Asp Thr Thr
        195                 200                 205

Gly Thr Asn Leu Phe Leu Val Ala Ala His Glu Ile Gly His Ser Leu
        210                 215                 220

Gly Leu Phe His Ser Ala Asn Thr Glu Ala Leu Met Tyr Pro Leu Tyr
225                 230                 235                 240

His Ser Leu Thr Asp Leu Thr Arg Phe Arg Leu Ser Gln Asp Asp Ile
                245                 250                 255

Asn Gly Ile Gln Ser Leu Tyr Gly Pro Pro Pro Asp Ser Pro Glu Thr
                260                 265                 270

Pro Leu Val Pro Thr Glu Pro Val Pro Pro Glu Pro Gly Thr Pro Ala
        275                 280                 285
```

16

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Asn Cys Asp Pro Ala Leu Ser Phe Asp Ala Val Ser Thr Leu Arg Gly
    290                 295                 300

Glu Ile Leu Ile Phe Lys Asp Arg His Phe Trp Arg Lys Ser Leu Arg
305                 310                 315                 320

Lys Leu Glu Pro Glu Leu His Leu Ile Ser Ser Phe Trp Pro Ser Leu
                325                 330                 335

Pro Ser Gly Val Asp Ala Ala Tyr Glu Val Thr Ser Lys Asp Leu Val
                340                 345                 350

Phe Ile Phe Lys Gly Asn Gln Phe Trp Ala Ile Arg Gly Asn Glu Val
        355                 360                 365

Arg Ala Gly Tyr Pro Arg Gly Ile His Thr Leu Gly Phe Pro Pro Thr
    370                 375                 380

Val Arg Lys Ile Asp Ala Ala Ile Ser Asp Lys Glu Lys Asn Lys Thr
385                 390                 395                 400

Tyr Phe Phe Val Glu Asp Lys Tyr Trp Arg Phe Asp Glu Lys Arg Asn
                405                 410                 415

Ser Met Glu Pro Gly Phe Pro Lys Gln Ile Ala Glu Asp Phe Pro Gly
                420                 425                 430

Ile Asp Ser Lys Ile Asp Ala Val Phe Glu Glu Phe Gly Phe Phe Tyr
                435                 440                 445

Phe Phe Thr Gly Ser Ser Gln Leu Glu Phe Asp Pro Asn Ala Lys Lys
    450                 455                 460

Val Thr His Thr Leu Lys Ser Asn Ser Trp Leu Asn Cys
465                 470                 475


<210> 16
<211> 708
<212> PRT
<213> Unknown

<220>
<223> X = UNKNOWN

<220>
<223> Description of Unknown Organism: Known Member of
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Matrix Metalloproteinase Family

<400> 16
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Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1               5                   10                  15

Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
            20                  25                  30

Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
            35                  40                  45

Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
        50                  55                  60

Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65                  70                  75                  80

Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
                85                  90                  95

Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
            100                 105                 110

Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
            115                 120                 125

Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
        130                 135                 140

Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145                 150                 155                 160

Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
            165                 170                 175

Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
            180                 185                 190

Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
            195                 200                 205

Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
        210                 215                 220

Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225                 230                 235                 240
```

18

Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
              245   250   255

Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
              260   265   270

Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
        275   280   285

Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
        290   295   300

Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305   310   315   320

Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
              325   330   335

Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
              340   345   350

Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
              355   360   365

Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
        370   375   380

Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385   390   395   400

His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
              405   410   415

Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
              420   425   430

Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
        435   440   445

Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
        450   455   460

Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465   470   475   480

Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
              485   490   495

19

Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
        500   505   510

Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
        515   520   525

Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
        530   535   540

Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545   550   555   560

Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
                565   570   575

Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
                580   585   590

Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
        595   600   605

Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
        610   615   620

Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625   630   635   640

Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
                645   650   655

Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
                660   665   670

Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
        675   680   685

Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
        690   695   700

Pro Glu Asp Xaa
705

<210> 17
<211> 631
<212> PRT
<213> Unknown

20

<220>

<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 17
Ala Pro Ser Pro Ile Ile Lys Phe Pro Gly Asp Val Ala Pro Lys Thr
 1   5   10   15

Asp Lys Glu Leu Ala Val Gln Tyr Leu Asn Thr Phe Tyr Gly Cys Pro
             20   25   30

Lys Glu Ser Cys Asn Leu Phe Val Leu Lys Asp Thr Leu Lys Lys Met
         35   40   45

Gln Lys Phe Phe Gly Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr
     50   55   60

Ile Glu Thr Met Arg Lys Pro Arg Cys Gly Asn Pro Asp Val Ala Asn
 65   70   75   80

Tyr Asn Phe Phe Pro Arg Lys Pro Lys Trp Asp Lys Asn Gln Ile Thr
                 85   90   95

Tyr Arg Ile Ile Gly Tyr Thr Pro Asp Leu Asp Pro Glu Thr Val Asp
             100   105   110

Asp Ala Phe Ala Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro Leu
             115   120   125

Arg Phe Ser Arg Ile His Asp Gly Glu Ala Asp Ile Met Ile Asn Phe
     130   135   140

Gly Arg Trp Glu His Gly Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly
145   150   155   160

Leu Leu Ala His Ala Phe Ala Pro Gly Thr Gly Val Gly Gly Asp Ser
             165   170   175

His Phe Asp Asp Asp Glu Leu Trp Thr Leu Gly Glu Gly Gln Val Val
             180   185   190

Arg Val Lys Tyr Gly Asn Ala Asp Gly Glu Tyr Cys Lys Phe Pro Phe
             195   200   205

Leu Phe Asn Gly Lys Glu Tyr Asn Ser Cys Thr Asp Thr Gly Arg Ser
     210   215   220

Asp Gly Phe Leu Trp Cys Ser Thr Thr Tyr Asn Phe Glu Lys Asp Gly

21

Lys Tyr Gly Phe Cys Pro His Glu Ala Leu Phe Thr Met Gly Gly Asn
          245   250   255

Ala Glu Gly Gln Pro Cys Lys Phe Pro Phe Arg Phe Gln Gly Thr Ser
          260   265   270

Tyr Asp Ser Cys Thr Thr Glu Gly Arg Thr Asp Gly Tyr Arg Trp Cys
          275   280   285

Gly Thr Thr Glu Asp Tyr Asp Arg Asp Lys Lys Tyr Gly Phe Cys Pro
          290   295   300

Glu Thr Ala Met Ser Thr Val Gly Gly Asn Ser Glu Gly Ala Pro Cys
305   310   315   320

Val Phe Pro Phe Thr Phe Leu Gly Asn Lys Tyr Glu Ser Cys Thr Ser
          325   330   335

Ala Gly Arg Ser Asp Gly Lys Met Trp Cys Ala Thr Thr Ala Asn Tyr
          340   345   350

Asp Asp Asp Arg Lys Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu
          355   360   365

Phe Leu Val Ala Ala His Glu Phe Gly His Ala Met Gly Leu Glu His
          370   375   380

Ser Gln Asp Pro Gly Ala Leu Met Ala Pro Ile Tyr Thr Tyr Thr Lys
385   390   395   400

Asn Phe Arg Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Glu Leu Tyr
          405   410   415

Gly Ala Ser Pro Asp Ile Asp Leu Gly Thr Gly Pro Thr Pro Thr Leu
          420   425   430

Gly Pro Val Thr Pro Glu Ile Cys Lys Gln Asp Ile Val Phe Asp Gly
          435   440   445

Ile Ala Gln Ile Arg Gly Glu Ile Phe Phe Phe Lys Asp Arg Phe Ile
          450   455   460

Trp Arg Thr Val Thr Pro Arg Asp Lys Pro Met Gly Pro Leu Leu Val
465   470   475   480

Ala Thr Phe Trp Pro Glu Leu Pro Glu Lys Ile Asp Ala Val Tyr Glu

22

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                    485                    490                    495

Ala Pro Gln Glu Glu Lys Ala Val Phe Phe Ala Gly Asn Glu Tyr Trp
            500                    505                    510

Ile Tyr Ser Ala Ser Thr Leu Glu Arg Gly Tyr Pro Lys Pro Leu Thr
            515                    520                    525

Ser Leu Gly Leu Pro Pro Asp Val Gln Arg Val Asp Ala Ala Phe Asn
            530                    535                    540

Trp Ser Lys Asn Lys Lys Thr Tyr Ile Phe Ala Gly Asp Lys Phe Trp
545                    550                    555                    560

Arg Tyr Asn Glu Val Lys Lys Lys Met Asp Pro Gly Phe Pro Lys Leu
                565                    570                    575

Ile Ala Asp Ala Trp Asn Ala Ile Pro Asp Asn Leu Asp Ala Val Val
            580                    585                    590

Asp Leu Gln Gly Gly Gly His Ser Tyr Phe Phe Lys Gly Ala Tyr Tyr
            595                    600                    605

Leu Lys Leu Glu Asn Gln Ser Leu Lys Ser Val Lys Phe Gly Ser Ile
            610                    615                    620

Lys Ser Asp Trp Leu Gly Cys
625                    630


<210> 18
<211> 267
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Known Member of
      Matrix Metalloproteinase Family

<400> 18
Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu
 1               5                  10                    15

Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp
            20                    25                    30

Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
            35                    40                    45
```

23

Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
    50   55   60

Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
65   70   75   80

Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
                85   90   95

Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
                100   105   110

Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
                115   120   125

Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
    130   135   140

Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
145   150   155   160

Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
                165   170   175

Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
                180   185   190

Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
    195   200   205

Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
    210   215   220

Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp
225   230   235   240

Pro Gln Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys
                245   250   255

Leu Tyr Gly Lys Arg Ser Asn Ser Arg Lys Lys
                260   265

<210> 19
<211> 231
<212> PRT
<213> Unknown

24

<220>

<223> Description of Unknown Organism: Known Member of
Matrix Metalloproteinase Family

<400> 19

```
Met Pro Leu Leu Leu Leu Leu Glu Tyr Leu Glu Lys Leu Met Gln Lys
 1               5                  10                  15

Phe Gly Leu Val Thr Gly Lys Leu Asp Thr Leu Met Arg Lys Pro Arg
            20                  25                  30

Cys Gly Val Pro Asp Val Gly Phe Phe Pro Gly Pro Lys Trp Thr Leu
            35                  40                  45

Thr Tyr Arg Ile Asn Tyr Thr Pro Asp Leu Pro Val Asp Ala Lys Ala
            50                  55                  60

Phe Val Trp Ser Val Thr Pro Leu Thr Phe Arg Val Glu Gly Ala Asp
 65                  70                  75                  80

Ile Met Ile Phe Ala His Gly Asp Tyr Pro Phe Asp Gly Pro Gly Gly
                85                  90                  95

Leu Ala His Ala Phe Pro Gly Pro Gly Ile Gly Gly Asp Ala His Phe
            100                 105                 110

Asp Asp Glu Trp Thr Asn Leu Phe Leu Val Ala Ala His Glu Gly His
            115                 120                 125

Ser Leu Gly Leu His Ser Asp Pro Ala Leu Met Tyr Pro Thr Phe Phe
            130                 135                 140

Leu Ser Gln Asp Asp Ile Gly Ile Gln Leu Tyr Gly Pro Pro Thr Cys
145                 150                 155                 160

Asp Phe Asp Ala Ile Thr Arg Gly Glu Phe Phe Lys Asp Arg Trp Arg
                165                 170                 175

Leu Ser Phe Trp Pro Leu Pro Asp Ala Ala Tyr Glu Phe Phe Gly Asn
            180                 185                 190

Tyr Trp Gly Gly Tyr Pro Ile Leu Gly Pro Val Asp Ala Ala Lys Thr
            195                 200                 205

Tyr Phe Phe Lys Trp Arg Asp Met Pro Gly Pro Ile Phe Pro Gly Asp
    210                 215                 220
```

Ala Val Phe Phe Trp Leu Cys
225   230